

We claim:

1. The use of nuclear encoded Clp-protease in a method for identifying herbicides.
2. The use as claimed in claim 1, wherein the Clp-protease is
  - a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or
  - b) selected from the group consisting of ClpR1-protease, ClpR3-protease, ClpR4-protease; or
  - c) ClpP-like-protease.
3. A plant nucleic acid sequence encoding a ClpP2-protease comprising:
  - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or
  - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by backtranslating, or
  - c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of has at least 66%.
4. A plant nucleic acid sequence encoding a ClpR1-protease comprising:
  - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11, or
  - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by backtranslating, or
  - c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of has at least 69%.
5. A plant nucleic acid sequence encoding a ClpP-like-protease comprising:

- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or
- 5 b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by backtranslating, or
- c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of at least 67%.
- 10 6. A polypeptide with the activity of a nuclear encoded Clp-protease, encoded by a nucleic acid molecule as claimed in claim 3, 4 or 5.
- 15 7. An expression cassette comprising
- a) genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 3, 4 or 5; or
- 20 b) additional functional elements, or
- c) a combination of a) and b).
8. A vector comprising an expression cassette as claimed in claim 7.
- 25 9. A transgenic organism comprising at least one nucleic acid sequence as claimed in claim 4, 5 or 6 encoding a polypeptide with the activity of a Clp-protease, an expression cassette as claimed in claim 7 or a vector as claimed in claim 8, selected from among bacteria, yeasts, fungi, animal cells or plant cells.
- 30 10. A method for identifying substances with herbicidal activity, comprising the following steps:
- 35 i. bringing a nuclear encoded Clp-protease into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule encoding Clp-protease or to the nuclear encoded Clp-protease, and
- 40 ii. detecting whether the test compound binds to the Clp-protease of i), or
- iii. detecting whether the test compound reduces or blocks the enzymatic or biological activity of the Clp-protease of i), or

- iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the Clp-protease of i).

11. A method as claimed in claim 10, wherein the Clp-protease is

- a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or
- b) selected from the group consisting of ClpR1-protease, ClpR3-protease, ClpR4-protease; or
- c) ClpP-like-protease.

12. A method as claimed in claim 10, wherein

- a) the ClpP1-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or
- ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translating, or
- iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:1 which has an identity with SEQ ID NO:1 of has at least 50%;
- b) the ClpP2-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or
- ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by back translating, or
- iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of has at least 50%;

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- c) the ClpP3-protease is encoded by a nucleic acid sequence which comprises:
    - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5, or
    - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:6 by back translating, or
    - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:5 which has an identity with SEQ ID NO:5 of has at least 50%;
  - d) the ClpP4-protease is encoded by a nucleic acid sequence which comprises:
    - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:7, or
    - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:8 by back translating, or
    - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:7 which has an identity with SEQ ID NO:7 of has at least 50%;
  - e) the ClpP6-protease is encoded by a nucleic acid sequence which comprises:
    - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:9, or
    - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:10 by back translating, or
    - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:9 which has an identity with SEQ ID NO:9 of has at least 50%;
  - f) the ClpR1-protease is encoded by a nucleic acid sequence which comprises:

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- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11, or
  - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by back translating, or
  - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of has at least 50%;
- g) the ClpR3-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:13, or
  - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:14 by back translating, or
  - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:13 which has an identity with SEQ ID NO:13 of has at least 50%;
- h) the ClpR4-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:15, or
  - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:16 by back translating, or
  - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:15 which has an identity with SEQ ID NO:15 of has at least 50%;
- i) the ClpP like-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or

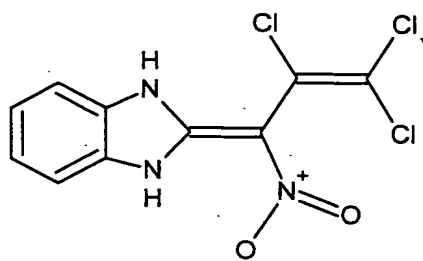
- ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by back translating, or
  - 5      iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of has at least 50%;
- 13. A method as claimed in claim 10, 11 or 12, wherein a test compound is selected which reduces or blocks the enzymatic or biological activity of Clp-protease.
- 10      14. A method as claimed in any of claims 10, 11, 12 or 13, wherein
  - i. either Clp-protease is expressed in a transgenic organism or an organism which naturally contains Clp-protease is grown,
  - 15      ii. the Clp-protease of step i) is brought into contact with a test compound in the cell digest of the transgenic or nontransgenic organism, in partially purified form or in homogeneously purified form, and
  - 20      iii. selecting a test compound which reduces or blocks the enzymatic activity of the Clp-protease of step a).
- 15. A method as claimed in any of claims 10, 11, 12 or 13, which comprises the following steps:
  - 25      i. generating a transgenic organism comprising a nucleic acid sequence encoding Clp-protease, wherein Clp-protease is expressed recombinantly;
  - 30      ii. applying a test substance to the transgenic organism of i) and to a non-transgenic organism of the same genotype,
  - 35      iii. determining the growth or the viability of the transgenic plant and the non-transgenic plant after application of the test compound, and
  - 40      iv. selecting test substances which bring about a reduced growth of the non-transgenic plant in comparison with the growth of the transgenic plant.
- 16. A method as claimed in claim 15, which is carried out in a plant organism, a cyanobacterium or proteobacterium.
- 17. A method for identifying substances with growth-regulatory activity, which comprises the following steps:

- i. generating a transgenic plant comprising a nucleic acid sequence Clp-protease, wherein Clp-protease is expressed recombinantly;
  - 5 ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same variety,
  - 10 iii. determining the growth or the viability of the transgenic plant and the non-transgenic plant after application of the test compound, and
  - iv. selecting test substances which bring about a reduced growth of the non-transgenic plant in comparison with the growth of the transgenic plant.
- 15 18. A method as claimed in any of claims 10 to 17, wherein the substances are identified in high-throughput screening method.
- 20 19. A support comprising one or more of the nucleic acid molecules as claimed in claim 3, 4, or 5 one or more expression cassettes as claimed in claim 7, one or more vectors as claimed in claim 8, one or more organisms as claimed in claim 9 or one or more (poly)peptides as claimed in claim 6.
- 25 20. A method as claimed in any of claims 10 to 18, wherein the substances are identified in High-Throughput Screening using a support as claimed in claim 19.
- 30 21. The use of a compound with herbicidal activity, identified by one of the methods as claimed in any of claims 10 to 16, 18 and 20 for controlling undesired vegetation and/or for regulating the growth of plants.
22. The use of a compound with growth-regulatory activity, identified by the method as claimed in any of claims 17, 18 or 20 for controlling undesired vegetation and/or for regulating the growth of plants.
- 35 23. A method for the preparation of an agrochemical composition, which comprises
- a) identifying a compound with herbicidal activity by one of the methods as claimed in any of claims 10 to 16, 18 and 20 or a compound with growth-regulatory activity as claimed in any of claims 17, 18 or 20, and
  - 40 b) formulating this compound together with suitable auxiliaries to give crop protection products with herbicidal or growth-regulatory activity.

24. The use of at least one Clp-protease inhibitor identified by one of the methods as claimed in any of claims 10 to 16, 18 and 20 in a method for controlling undesired vegetation and/or for regulating the growth of plants.

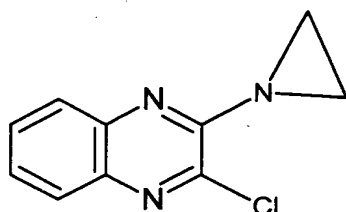
25. A method for controlling undesired vegetation and/or for regulating the growth of plants comprising treating said weeds with a herbicide, wherein said herbicide is a compound which is a inhibitor of a Clp-protease.

26. Clp-protease inhibitor of the formula:



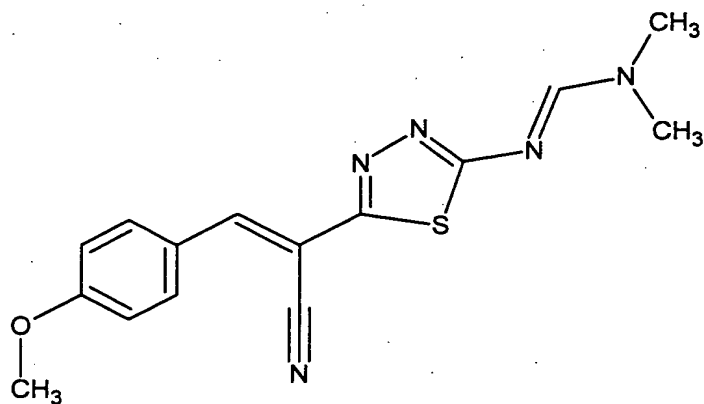
formula (I)

or



formula (II)

or



formula (III).